

SEQUENCE LISTING

<110> Raju, Jeyaseelan

<120> NOVEL CARK PROTEIN AND NUCLEIC ACID MOLECULES AND USES
THEREFOR

<130> MNI-068CP2

<140> US 09/947,199

<141> 2001-09-05

<150> US 60/111,938

<151> 1998-12-11

<150> US 09/291,839

<151> 1999-04-14

<150> US 09/458,457

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<170> PatentIn Ver. 2.0

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cag	gtt	gga	tac	ggg	ggc	ctc	act	gcc	ctc	cat	att	gct	aca	ata	gct	432	
Gln	Val	Gly	Tyr	Gly	Gly	Leu	Thr	Ala	Leu	His	Ile	Ala	Thr	Ile	Ala		
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Gly	His	Leu	Glu	Ala	Ala	Asp	Val	Leu	Leu	Gln	His	Gly	Ala	Asn	Val		
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Asn	Ile	Gln	Asp	Ala	Val	Phe	Phe	Thr	Pro	Leu	His	Ile	Ala	Ala	Tyr		
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tat	gga	cat	gaa	cag	gta	act	cgc	ctt	ctt	ttg	aaa	ttt	ggg	gct	gat	576	
Tyr	Gly	His	Glu	Gln	Val	Thr	Arg	Leu	Leu	Leu	Lys	Phe	Gly	Ala	Asp		
			180					185					190				
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Val	Asn	Val	Ser	Gly	Glu	Val	Gly	Asp	Arg	Pro	Leu	His	Leu	Ala	Ser		
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gca	aaa	gga	ttc	ttg	aat	att	gca	aaa	ctc	ttg	atg	gaa	gaa	ggc	agc	672	
Ala	Lys	Gly	Phe	Leu	Asn	Ile	Ala	Lys	Leu	Leu	Met	Glu	Glu	Gly	Ser		
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Lys	Ala	Asp	Val	Asn	Ala	Gln	Asp	Asn	Glu	Asp	His	Val	Pro	Leu	His		
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Phe	Cys	Ser	Arg	Phe	Gly	His	His	Asp	Ile	Val	Lys	Tyr	Leu	Leu	Gln		
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Ser	Asp	Leu	Glu	Val	Gln	Pro	His	Val	Val	Asn	Ile	Tyr	Gly	Asp	Thr	
			260					265					270			
ccc	tta	cac	ctg	gca	tgc	tac	aat	ggc	aaa	ttt	gaa	gtt	gcc	aag	gaa	864
Pro	Leu	His	Leu	Ala	Cys	Tyr	Asn	Gly	Lys	Phe	Glu	Val	Ala	Lys	Glu	
		275					280				285					
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Ile	Ile	Gln	Ile	Ser	Gly	Thr	Glu	Ser	Leu	Thr	Lys	Glu	Asn	Ile	Phe	
	290					295				300						
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Ser	Glu	Thr	Ala	Phe	His	Ser	Ala	Cys	Thr	Tyr	Gly	Lys	Ser	Ile	Asp	
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cta	gtc	aaa	ttt	ctt	ctt	gat	cag	aat	gtc	ata	aac	atc	aac	cac	caa	1008
Leu	Val	Lys	Phe	Leu	Leu	Asp	Gln	Asn	Val	Ile	Asn	Ile	Asn	His	Gln	
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gga	agg	gat	ggg	cac	act	gga	tta	cac	tct	gct	tgc	tac	cac	ggg	cac	1056
Gly	Arg	Asp	Gly	His	Thr	Gly	Leu	His	Ser	Ala	Cys	Tyr	His	Gly	His	
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Ile	Arg	Leu	Val	Gln	Phe	Leu	Leu	Asp	Asn	Gly	Ala	Asp	Met	Asn	Leu	
		355				360						365				
gtg	gct	tgt	gat	ccc	agc	agg	tct	agt	ggg	gaa	aaa	gat	gag	cag	aca	1152
Val	Ala	Cys	Asp	Pro	Ser	Arg	Ser	Ser	Gly	Glu	Lys	Asp	Glu	Gln	Thr	
	370					375					380					
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Cys	Leu	Met	Trp	Ala	Tyr	Glu	Lys	Gly	His	Asp	Ala	Ile	Val	Thr	Leu	
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Leu	Lys	His	Tyr	Lys	Arg	Pro	Gln	Asp	Glu	Leu	Pro	Cys	Asn	Glu	Tyr	
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Ser	Gln	Pro	Gly	Gly	Asp	Gly	Ser	Tyr	Val	Ser	Val	Pro	Ser	Pro	Leu	
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Gly	Lys	Ile	Lys	Ser	Met	Thr	Lys	Glu	Lys	Ala	Asp	Ile	Leu	Leu	Leu	
	435						440					445				
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Arg	Ala	Gly	Leu	Pro	Ser	His	Phe	His	Leu	Gln	Leu	Ser	Glu	Ile	Glu	
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Phe	His	Glu	Ile	Ile	Gly	Ser	Gly	Ser	Phe	Gly	Lys	Val	Tyr	Lys	Gly	
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Arg	Cys	Arg	Asn	Lys	Ile	Val	Ala	Ile	Lys	Arg	Tyr	Arg	Ala	Asn	Thr	
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Tyr	Cys	Ser	Lys	Ser	Asp	Val	Asp	Met	Phe	Cys	Arg	Glu	Val	Ser	Ile	
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Leu	Cys	Gln	Leu	Asn	His	Pro	Cys	Val	Ile	Gln	Phe	Val	Gly	Ala	Cys	
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Gly	Ser	Leu	Phe	Ser	Leu	Leu	His	Glu	Gln	Lys	Arg	Ile	Leu	Asp	Leu	
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cag	tct	aaa	tta	att	att	gca	gta	gat	gtt	gcc	aaa	ggc	atg	gag	tac	1728
Gln	Ser	Lys	Leu	Ile	Ile	Ala	Val	Asp	Val	Ala	Lys	Gly	Met	Glu	Tyr	
			565					570						575		
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Leu	His	Asn	Leu	Thr	Gln	Pro	Ile	Ile	His	Arg	Asp	Leu	Asn	Ser	His	
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aat	att	ctt	ctc	tat	gag	gat	ggg	cat	gct	gtg	gtg	gca	gat	ttt	gga	1824
Asn	Ile	Leu	Leu	Tyr	Glu	Asp	Gly	His	Ala	Val	Val	Ala	Asp	Phe	Gly	
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Glu	Ser	Arg	Phe	Leu	Gln	Ser	Leu	Asp	Glu	Asp	Asn	Met	Thr	Lys	Gln	
	610					615					620					
cct	ggg	aac	ctc	cgt	tgg	atg	gct	cct	gag	gtg	ttc	acg	cag	tgc	act	1920
Pro	Gly	Asn	Leu	Arg	Trp	Met	Ala	Pro	Glu	Val	Phe	Thr	Gln	Cys	Thr	
625					630					635					640	
cgg	tac	acc	atc	aaa	gca	gat	gtc	ttc	agc	tat	gct	ctg	tgt	ctg	tgg	1968
Arg	Tyr	Thr	Ile	Lys	Ala	Asp	Val	Phe	Ser	Tyr	Ala	Leu	Cys	Leu	Trp	
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gaa	att	ctc	act	ggc	gaa	att	cca	ttc	gct	cat	ctc	aag	cca	gcg	gct	2016
Glu	Ile	Leu	Thr	Gly	Glu	Ile	Pro	Phe	Ala	His	Leu	Lys	Pro	Ala	Ala	
		660					665						670			
gcg	gca	gca	gac	atg	gct	tac	cac	cac	atc	aga	cct	ccc	att	ggc	tat	2064
Ala	Ala	Ala	Asp	Met	Ala	Tyr	His	His	Ile	Arg	Pro	Pro	Ile	Gly	Tyr	
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tcc	att	ccc	aag	ccc	ata	tca	tct	ctg	ctg	ata	cga	ggg	tgg	aac	gca	2112
Ser	Ile	Pro	Lys	Pro	Ile	Ser	Ser	Leu	Leu	Ile	Arg	Gly	Trp	Asn	Ala	
	690					695					700					
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12

Cys	Pro	Glu	Gly	Arg	Pro	Glu	Phe	Ser	Glu	Val	Val	Met	Lys	Leu	Glu	
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	770					775					780					
gct gga caa tat tcc tct caa ggt ctg tct ttg gag gag atg aaa aga 2400																
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785					790					795					800	
agt ctt caa tac aca ccc att gac aaa tat ggc tat gta tcc gat ccc 2448																
Ser	Leu	Gln	Tyr	Thr	Pro	Ile	Asp	Lys	Tyr	Gly	Tyr	Val	Ser	Asp	Pro	
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Met	Ser	Ser	Met	His	Phe	His	Ser	Cys	Arg	Asn	Ser	Ser	Ser	Phe	Glu	
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<211> 34

<212> PRT

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<220>

<221> VARIANT

<222> 3

<223> Xaa = any amino acid except Pro

<220>

<221> VARIANT

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<223> Xaa = any amino acid except Pro

<220>
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<223> Xaa = Phe, Tyr, Trp, Met, Gly, Ser, Thr, Asn,
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<220>
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<220>
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<223> Any 13 Xaa's may be absent - represents a range
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<223> Xaa = Leu, Ile, Val, Met, Phe, Tyr, Trp, Cys, Ser,
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<220>
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Xaa Lys

<210> 5
 <211> 13
 <212> PRT
 <213> Artificial Sequence

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<220>
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 <222> 3
 <223> Xaa = His or Tyr

<220>
 <221> ACT_SITE
 <222> 5
 <223> Asp is an active site residue

<220>
 <221> VARIANT
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<220>
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<223> Xaa = His or Tyr

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<223> Asp is an active site residue

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<223> Xaa = Leu, Ile, Val, Met, Phe, Tyr

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<223> Xaa = Arg, Ser, Thr, Ala, or Cys

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atg ggg aat tac aaa tcc aga cca aca cag act tgt tct gat gaa tgg 108
 Met Gly Asn Tyr Lys Ser Arg Pro Thr Gln Thr Cys Ser Asp Glu Trp
 1 5 10 15

aag aag aaa gtt agt gaa tct tac gct att atc ata gaa agg ctg gag 156
 Lys Lys Lys Val Ser Glu Ser Tyr Ala Ile Ile Ile Glu Arg Leu Glu
 20 25 30

gat aac ctg cag atc aaa gaa aat gaa ttt caa gaa cta agg cac atc 204
 Asp Asn Leu Gln Ile Lys Glu Asn Glu Phe Gln Glu Leu Arg His Ile
 35 40 45

ttt ggc tct gat gaa gcc ttc agt gaa gtc agt tta aat tac cgc aca 252
 Phe Gly Ser Asp Glu Ala Phe Ser Glu Val Ser Leu Asn Tyr Arg Thr
 50 55 60

gag cgt ggc ctg tcc ctg cta cac ctc tgc tgt gtc tgt ggc ggc aac 300
 Glu Arg Gly Leu Ser Leu Leu His Leu Cys Cys Val Cys Gly Gly Asn
 65 70 75 80

aag tca cat atc cgt gcc ctt atg tta aaa ggg ctc cgt cca tcc aga 348
 Lys Ser His Ile Arg Ala Leu Met Leu Lys Gly Leu Arg Pro Ser Arg
 85 90 95

ctg acg aga aat ggg ttt cca gct ctg cac ctg gcc gtt tac aag gac 396
 Leu Thr Arg Asn Gly Phe Pro Ala Leu His Leu Ala Val Tyr Lys Asp
 100 105 110

agc ccg gaa ctt atc act tca ctg ttg cac agc gga gca gat gtt cag 444
 Ser Pro Glu Leu Ile Thr Ser Leu Leu His Ser Gly Ala Asp Val Gln
 115 120 125

caa gtg gga tac ggt ggc ctc aca gcc ctc cac ata gct gca ata gct 492
 Gln Val Gly Tyr Gly Gly Leu Thr Ala Leu His Ile Ala Ala Ile Ala
 130 135 140

gga cac cca gag gct gca gaa gtg ctg cta caa cat ggg gcc aat gtg 540
 Gly His Pro Glu Ala Ala Glu Val Leu Leu Gln His Gly Ala Asn Val
 145 150 155 160

aat gtt caa gat gcc gtc ttc ttc acc cca ctg cac att gca gcc tac 588
 Asn Val Gln Asp Ala Val Phe Phe Thr Pro Leu His Ile Ala Ala Tyr
 165 170 175

tat ggg cac gag cag gta acc agt gtc ctt ttg aag ttt ggt gct gat	636
Tyr Gly His Glu Gln Val Thr Ser Val Leu Leu Lys Phe Gly Ala Asp	
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Val Asn Val Ser Gly Glu Val Gly Asp Arg Pro Leu His Leu Ala Ser	
195 200 205	
gca aag ggc ttc ttc aac att gtg aaa ctc ctg gta gaa gaa ggg agc	732
Ala Lys Gly Phe Phe Asn Ile Val Lys Leu Leu Val Glu Glu Gly Ser	
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Lys Ala Asp Val Asn Ala Gln Asp Asn Glu Asp His Val Pro Leu His	
225 230 235 240	
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Phe Cys Ser Arg Phe Gly His His Asn Ile Val Ser Tyr Leu Leu Gln	
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agt gac tta gag gtc cag cct cac gtc att aac atc tat ggt gac act	876
Ser Asp Leu Glu Val Gln Pro His Val Ile Asn Ile Tyr Gly Asp Thr	
260 265 270	
cct ttg cac ctg gca tgc tac aat gga aat ttt gaa gtt gcc aag gaa	924
Pro Leu His Leu Ala Cys Tyr Asn Gly Asn Phe Glu Val Ala Lys Glu	
275 280 285	
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Ile Val Gln Val Thr Gly Thr Glu Ser Leu Thr Lys Glu Asn Ile Phe	
290 295 300	
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Ser Glu Thr Ala Phe His Ser Ala Cys Thr Tyr Gly Lys Asn Ile Asp	
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Val Ala Cys Asp Pro Ser Arg Ser Ser Gly Glu Lys Asp Glu Gln Thr	
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Cys Leu Met Trp Ala Tyr Glu Lys Gly His Asp Ala Ile Val Thr Leu	
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Leu Lys His Tyr Lys Arg Pro Gln Glu Glu Leu Pro Cys Asn Glu Tyr	
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Gly Lys Ile Lys Ser Met Thr Lys Glu Lys Ala Asp Val Leu Leu Leu	
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Arg Ala Glu Leu Pro Ser Arg Phe His Leu Gln Leu Ser Glu Ile Glu	
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Phe His Glu Ile Ile Gly Ser Gly Ser Phe Gly Lys Val Tyr Lys Gly	
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Arg Cys Arg Asn Lys Ile Val Ala Ile Lys Arg Tyr Arg Ala Asn Thr	
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Tyr Cys Ser Lys Ser Asp Val Asp Met Phe Cys Arg Glu Val Ser Ile	
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Leu Cys Gln Leu Asn His Pro Cys Val Val Gln Phe Val Gly Ala Cys	
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ctg gat gac ccc agt cag ttt gcc att gtc act cag tac att tca gga	1692
Leu Asp Asp Pro Ser Gln Phe Ala Ile Val Thr Gln Tyr Ile Ser Gly	
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Gly Ser Leu Phe Ser Leu Leu His Glu Gln Lys Arg Ile Leu Asp Leu	
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Gln Ser Lys Leu Ile Ile Ala Val Asp Val Ala Lys Gly Met Glu Tyr	
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ctg cac agc ttg acc cag cca atc ata cac cgc gac ctg aac agc cac	1836
Leu His Ser Leu Thr Gln Pro Ile Ile His Arg Asp Leu Asn Ser His	
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Asn Ile Leu Leu Tyr Glu Asp Gly His Ala Val Val Ala Asp Phe Gly	
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Glu Ser Arg Phe Leu Gln Ser Leu Asp Glu Asp Asn Met Thr Lys Gln	
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Pro Gly Asn Leu Arg Trp Met Ala Pro Glu Val Phe Thr Gln Cys Thr	
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aga tac acc atc aag gct gat gtc ttc agt tac tcc ctg tgt ctg tgg	2028
Arg Tyr Thr Ile Lys Ala Asp Val Phe Ser Tyr Ser Leu Cys Leu Trp	
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gag ctc ctc act gga gaa att cca ttc gct cat ctc aag cca gcc gct	2076
Glu Leu Leu Thr Gly Glu Ile Pro Phe Ala His Leu Lys Pro Ala Ala	
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Ala Ala Ala Asp Met Ala Tyr His His Ile Arg Pro Pro Ile Gly Tyr	
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Ser Ile Pro Lys Pro Ile Ser Ser Leu Leu Ile Arg Gly Trp Asn Ala	
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Cys Pro Glu Gly Arg Pro Glu Phe Ser Glu Val Val Ser Lys Leu Glu	
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Glu Cys Leu Cys Asn Val Glu Leu Met Ser Pro Ala Ser Ser Asn Ser	
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Ser Gly Ser Leu Ser Pro Ser Ser Ser Ser Asp Cys Leu Leu Ser Arg	
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Gly Gly Pro Gly Arg Ser His Val Ala Ala Leu Arg Ser Arg Phe Glu	
755 760 765	
ttg gag tat gcc cta aat gca agg tcc tat gct ggg tgg tcc caa agt	2412
Leu Glu Tyr Ala Leu Asn Ala Arg Ser Tyr Ala Gly Trp Ser Gln Ser	
770 775 780	
gtt gga aca cac tct aat ccg ggc ctg tct ttg gag gag atg aat agg	2460
Val Gly Thr His Ser Asn Pro Gly Leu Ser Leu Glu Glu Met Asn Arg	
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Ser Thr Gln Tyr Ser Thr Val Asp Lys Tyr Gly Tyr Val Ser Asp Pro	
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Met Ser Leu Thr His Leu His Ser Arg Gln Asp Asp Ser Asn Phe Glu	
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Asp Ser Asn	
835	

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 ggctttgact catgccaagc ctgaagtgtc aaagagcaga tacagaatgt gcatgaggaa 2785
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 35 40 45
 Phe Gly Ser Asp Glu Ala Phe Ser Glu Val Ser Leu Asn Tyr Arg Thr
 50 55 60
 Glu Arg Gly Leu Ser Leu Leu His Leu Cys Cys Val Cys Gly Gly Asn
 65 70 75 80
 Lys Ser His Ile Arg Ala Leu Met Leu Lys Gly Leu Arg Pro Ser Arg
 85 90 95
 Leu Thr Arg Asn Gly Phe Pro Ala Leu His Leu Ala Val Tyr Lys Asp
 100 105 110
 Ser Pro Glu Leu Ile Thr Ser Leu Leu His Ser Gly Ala Asp Val Gln
 115 120 125
 Gln Val Gly Tyr Gly Gly Leu Thr Ala Leu His Ile Ala Ala Ile Ala
 130 135 140
 Gly His Pro Glu Ala Ala Glu Val Leu Leu Gln His Gly Ala Asn Val
 145 150 155 160
 Asn Val Gln Asp Ala Val Phe Phe Thr Pro Leu His Ile Ala Ala Tyr
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Tyr Gly His Glu Gln Val Thr Ser Val Leu Leu Lys Phe Gly Ala Asp
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 Val Asn Val Ser Gly Glu Val Gly Asp Arg Pro Leu His Leu Ala Ser
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 Ala Lys Gly Phe Phe Asn Ile Val Lys Leu Leu Val Glu Glu Gly Ser
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 Lys Ala Asp Val Asn Ala Gln Asp Asn Glu Asp His Val Pro Leu His
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 Phe Cys Ser Arg Phe Gly His His Asn Ile Val Ser Tyr Leu Leu Gln
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 Ser Asp Leu Glu Val Gln Pro His Val Ile Asn Ile Tyr Gly Asp Thr
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 Pro Leu His Leu Ala Cys Tyr Asn Gly Asn Phe Glu Val Ala Lys Glu
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 Ile Val Gln Val Thr Gly Thr Glu Ser Leu Thr Lys Glu Asn Ile Phe
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 Ser Glu Thr Ala Phe His Ser Ala Cys Thr Tyr Gly Lys Asn Ile Asp
 305 310 315 320
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 Gly Arg Asp Gly His Thr Gly Leu His Ser Ala Cys Tyr His Gly His
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 Ile Arg Leu Val Gln Phe Leu Leu Asp Asn Gly Ala Asp Met Asn Leu
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 Val Ala Cys Asp Pro Ser Arg Ser Ser Gly Glu Lys Asp Glu Gln Thr
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 Cys Leu Met Trp Ala Tyr Glu Lys Gly His Asp Ala Ile Val Thr Leu
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 Leu Lys His Tyr Lys Arg Pro Gln Glu Glu Leu Pro Cys Asn Glu Tyr
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 Ser Gln Pro Gly Gly Asp Gly Ser Tyr Val Ser Val Pro Ser Pro Leu
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 Gly Lys Ile Lys Ser Met Thr Lys Glu Lys Ala Asp Val Leu Leu Leu
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Tyr Cys Ser Lys Ser Asp Val Asp Met Phe Cys Arg Glu Val Ser Ile						
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Leu Cys Gln Leu Asn His Pro Cys Val Val Gln Phe Val Gly Ala Cys						
		515		520		525
Leu Asp Asp Pro Ser Gln Phe Ala Ile Val Thr Gln Tyr Ile Ser Gly						
		530		535		540
Gly Ser Leu Phe Ser Leu Leu His Glu Gln Lys Arg Ile Leu Asp Leu						
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Gln Ser Lys Leu Ile Ile Ala Val Asp Val Ala Lys Gly Met Glu Tyr						
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Leu His Ser Leu Thr Gln Pro Ile Ile His Arg Asp Leu Asn Ser His						
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Asn Ile Leu Leu Tyr Glu Asp Gly His Ala Val Val Ala Asp Phe Gly						
		595		600		605
Glu Ser Arg Phe Leu Gln Ser Leu Asp Glu Asp Asn Met Thr Lys Gln						
		610		615		620
Pro Gly Asn Leu Arg Trp Met Ala Pro Glu Val Phe Thr Gln Cys Thr						
625		630		635		640
Arg Tyr Thr Ile Lys Ala Asp Val Phe Ser Tyr Ser Leu Cys Leu Trp						
		645		650		655
Glu Leu Leu Thr Gly Glu Ile Pro Phe Ala His Leu Lys Pro Ala Ala						
		660		665		670
Ala Ala Ala Asp Met Ala Tyr His His Ile Arg Pro Pro Ile Gly Tyr						
		675		680		685
Ser Ile Pro Lys Pro Ile Ser Ser Leu Leu Ile Arg Gly Trp Asn Ala						
		690		695		700
Cys Pro Glu Gly Arg Pro Glu Phe Ser Glu Val Val Ser Lys Leu Glu						
705		710		715		720
Glu Cys Leu Cys Asn Val Glu Leu Met Ser Pro Ala Ser Ser Asn Ser						
		725		730		735
Ser Gly Ser Leu Ser Pro Ser Ser Ser Ser Asp Cys Leu Leu Ser Arg						
		740		745		750
Gly Gly Pro Gly Arg Ser His Val Ala Ala Leu Arg Ser Arg Phe Glu						
		755		760		765

Leu Glu Tyr Ala Leu Asn Ala Arg Ser Tyr Ala Gly Trp Ser Gln Ser
770 775 780

Val Gly Thr His Ser Asn Pro Gly Leu Ser Leu Glu Glu Met Asn Arg
785 790 795 800

Ser Thr Gln Tyr Ser Thr Val Asp Lys Tyr Gly Tyr Val Ser Asp Pro
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aag aag aaa gtt agt gaa tct tac gct att atc ata gaa agg ctg gag 96
Lys Lys Lys Val Ser Glu Ser Tyr Ala Ile Ile Ile Glu Arg Leu Glu
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gat aac ctg cag atc aaa gaa aat gaa ttt caa gaa cta agg cac atc 144
Asp Asn Leu Gln Ile Lys Glu Asn Glu Phe Gln Glu Leu Arg His Ile
35 40 45

ttt ggc tct gat gaa gcc ttc agt gaa gtc agt tta aat tac cgc aca 192
Phe Gly Ser Asp Glu Ala Phe Ser Glu Val Ser Leu Asn Tyr Arg Thr
50 55 60

gag cgt ggc ctg tcc ctg cta cac ctc tgc tgt gtc tgt ggc ggc aac 240
Glu Arg Gly Leu Ser Leu Leu His Leu Cys Cys Val Cys Gly Gly Asn
65 70 75 80

aag tca cat atc cgt gcc ctt atg tta aaa ggg ctc cgt cca tcc aga 288
Lys Ser His Ile Arg Ala Leu Met Leu Lys Gly Leu Arg Pro Ser Arg
85 90 95

ctg acg aga aat ggg ttt cca gct ctg cac ctg gcc gtt tac aag gac 336
Leu Thr Arg Asn Gly Phe Pro Ala Leu His Leu Ala Val Tyr Lys Asp
100 105 110

agc ccg gaa ctt atc act tca ctg ttg cac agc gga gca gat gtt cag 384
Ser Pro Glu Leu Ile Thr Ser Leu Leu His Ser Gly Ala Asp Val Gln

115	120	125	
caa gtg gga tac ggt ggc ctc	aca gcc ctc cac ata gct gca ata gct		432
Gln Val Gly Tyr Gly Gly Leu Thr Ala Leu His Ile Ala Ala Ile Ala			
130	135	140	
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Gly His Pro Glu Ala Ala Glu Val Leu Leu Gln His Gly Ala Asn Val			
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aat gtt caa gat gcc gtc ttc ttc acc cca ctg cac att gca gcc tac			528
Asn Val Gln Asp Ala Val Phe Phe Thr Pro Leu His Ile Ala Ala Tyr			
165	170	175	
tat ggg cac gag cag gta acc agt gtc ctt ttg aag ttt ggt gct gat			576
Tyr Gly His Glu Gln Val Thr Ser Val Leu Leu Lys Phe Gly Ala Asp			
180	185	190	
gtc aat gta agc ggt gaa gtt ggg gac agg cct ctg cac ctg gcc tct			624
Val Asn Val Ser Gly Glu Val Gly Asp Arg Pro Leu His Leu Ala Ser			
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Ala Lys Gly Phe Phe Asn Ile Val Lys Leu Leu Val Glu Glu Gly Ser			
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Lys Ala Asp Val Asn Ala Gln Asp Asn Glu Asp His Val Pro Leu His			
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ttc tgt tct cga ttt gga cac cac aat ata gtg agc tac ctg ctc cag			768
Phe Cys Ser Arg Phe Gly His His Asn Ile Val Ser Tyr Leu Leu Gln			
245	250	255	
agt gac tta gag gtc cag cct cac gtc att aac atc tat ggt gac act			816
Ser Asp Leu Glu Val Gln Pro His Val Ile Asn Ile Tyr Gly Asp Thr			
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cct ttg cac ctg gca tgc tac aat gga aat ttt gaa gtt gcc aag gaa			864
Pro Leu His Leu Ala Cys Tyr Asn Gly Asn Phe Glu Val Ala Lys Glu			
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Ile Val Gln Val Thr Gly Thr Glu Ser Leu Thr Lys Glu Asn Ile Phe			
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agc gag aca gct ttt cac agt gct tgt acc tat ggc aag aac att gac			960
Ser Glu Thr Ala Phe His Ser Ala Cys Thr Tyr Gly Lys Asn Ile Asp			
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ctg gtc aaa ttt ctt ctt gat cag aat gct gtg aac att aac cac cga			1008
Leu Val Lys Phe Leu Leu Asp Gln Asn Ala Val Asn Ile Asn His Arg			
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gga aga gat ggg cac aca gga ttg cac tct gct tgc tac cac ggc cat			1056
Gly Arg Asp Gly His Thr Gly Leu His Ser Ala Cys Tyr His Gly His			

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Ile	Arg	Leu	Val	Gln	Phe	Leu	Leu	Asp	Asn	Gly	Ala	Asp	Met	Asn	Leu															
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Val	Ala	Cys	Asp	Pro	Ser	Arg	Ser	Ser	Gly	Glu	Lys	Asp	Glu	Gln	Thr															
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Cys	Leu	Met	Trp	Ala	Tyr	Glu	Lys	Gly	His	Asp	Ala	Ile	Val	Thr	Leu															
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Leu	His	Ser	Leu	Thr	Gln	Pro	Ile	Ile	His	Arg	Asp	Leu	Asn	Ser	His	
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Asn	Ile	Leu	Leu	Tyr	Glu	Asp	Gly	His	Ala	Val	Val	Ala	Asp	Phe	Gly	
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Arg	Tyr	Thr	Ile	Lys	Ala	Asp	Val	Phe	Ser	Tyr	Ser	Leu	Cys	Leu	Trp	
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gag	ctc	ctc	act	gga	gaa	att	cca	ttc	gct	cat	ctc	aag	cca	gcc	gct	2016
Glu	Leu	Leu	Thr	Gly	Glu	Ile	Pro	Phe	Ala	His	Leu	Lys	Pro	Ala	Ala	
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gca	gca	gca	gat	atg	gcg	tat	cac	cac	atc	aga	ccg	ccc	atc	ggc	tat	2064
Ala	Ala	Ala	Asp	Met	Ala	Tyr	His	His	Ile	Arg	Pro	Pro	Ile	Gly	Tyr	
		675					680					685				
tcc	atc	ccc	aag	ccc	atc	tca	tcc	ctg	ctg	ata	cgg	ggc	tgg	aat	gca	2112
Ser	Ile	Pro	Lys	Pro	Ile	Ser	Ser	Leu	Leu	Ile	Arg	Gly	Trp	Asn	Ala	
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Cys	Pro	Glu	Gly	Arg	Pro	Glu	Phe	Ser	Glu	Val	Val	Ser	Lys	Leu	Glu	
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Glu	Cys	Leu	Cys	Asn	Val	Glu	Leu	Met	Ser	Pro	Ala	Ser	Ser	Asn	Ser	
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Ser	Gly	Ser	Leu	Ser	Pro	Ser	Ser	Ser	Ser	Asp	Cys	Leu	Leu	Ser	Arg	
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Gly	Gly	Pro	Gly	Arg	Ser	His	Val	Ala	Ala	Leu	Arg	Ser	Arg	Phe	Glu	
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Leu	Glu	Tyr	Ala	Leu	Asn	Ala	Arg	Ser	Tyr	Ala	Gly	Trp	Ser	Gln	Ser	
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Val	Gly	Thr	His	Ser	Asn	Pro	Gly	Leu	Ser	Leu	Glu	Glu	Met	Asn	Arg	

27

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gac agc aac	2505						
Asp Ser Asn							
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